5, 1998, and issued on February 29, 2000 as U.S. Pat. No. 6,030,784, which is a divisional of application serial No. 08/544,577, which was filed October 17, 1995, and issued on September 15, 1998 as U.S. Pat. No. 5,807,680, which is a divisional of application serial No. 08/152,482, which was filed November 12, 1993, and issued on October 17, 1995 as U.S. Pat. No. 5,459, 037.--

At page 7, line 28, please substitute the following paragraph for the previous version:

It is unlikely that all mRNAs are amenable to detection by this method for the following reasons. For an mRNA to surface in such a survey, it must be prevalent enough to produce a signal on the autoradiograph and contain a sequence in its 3′ 500 nucleotides capable of serving as a site for mismatched primer binding and priming. The more prevalent an individual mRNA species, the more likely it would be to generate a product. Thus, prevalent species may give bands with many different arbitrary primers. Because this latter property would contain an unpredictable element of chance based on selection of the arbitrary primers, it would be difficult to approach closure by the arbitrary primer method. Also, for the information to be portable from one laboratory to another and reliable, the mismatched priming must be highly reproducible under different laboratory conditions using different PCR machines, with the resulting slight variation in reaction conditions. As the basis for mismatched priming is poorly understood, this is a drawback of building a database from data obtained by the Liang & Pardee differential display method.

At page 12, line 13, please insert

--Typically, in the present method the intensity of each band displayed after electrophoresis is about proportional to the abundance of the mRNA corresponding to the band in the original mixture. Typically the present method further comprises a step of determining the

relative abundance of each mRNA in the original mixture from the intensity of the band corresponding to that mRNA after electrophoresis.--

B3

Replacement with PP #7

IN THE SEQUENCE LISTING

Please delete the SEQUENCE LISTING on pages 41-45 and replace with

-- SEQUENCE LISTING

<110> Sutcliffe, J. G.
Erlander, Mark G.

<120> Method for Simultaneous Identification of Differentially Expressed mRNAs and Measurement of Relative Concentrations

<130> TSRI 401.0D3

<140>
<141>

<150> US 08/152,482
<151> 1993-11-12

<150> US 08/544,577
<151> 1995-10-17

<150> US 09/035,190
<151> 1998-03-05

<160> 6

<170> PatentIn Ver. 2.0

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<223> Description of Artificial Sequence:synthetic primer

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<212> DNA
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<223> Description of Artificial Sequence:synthetic primer

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aggtcgacgg tatcggnnnn 20--

IN THE CLAIMS

Please cancel claims 1-13 and 18-37. Please amend claims 14-17 to read as follows:

14. A method for recognizing sequence identities and similarities between the sequence of a cDNA fragment corresponding to a mRNA molecule present in a sample and a database of sequences, comprising the steps of:

eluting a cDNA fragment corresponding to a mRNA molecule present in a sample;

amplifying the eluted cDNA fragment in a polymerase chain reaction to produce